

REMARKS

In response to the Notice of Defective Response, a copy of the substitute sequence listing in computer readable form is attached hereto. The content of the paper copy of the sequence listing and the copy of the sequence listing in computer readable form is the same, and includes no new matter.

It is believed that by submitting the present amendment and the sequence listing diskette, the application now fully complies with the requirements of 37 CFR §§ 1.821-1.825. Applicants respectfully solicit issuance of the patent.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such deposit account.

Respectfully submitted,  
KEIL & WEINKAUF



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## SEQUENCE LISTING

<110> Kock, Michael  
 Hoeger, Thomas  
 Kroeger, Burkhard  
 Otterbach, Bernd  
 Lubisch, Wilfried  
 Lemaire, Hans-Georg

<120> Poly (ADP-ribose) polymerase-gene

<130> 0050/49100

<140> US 09/701,586  
 <141> 1999-06-04

<150> PCT/EP99/03889  
 <151> 1999-06-04

<160> 33

<170> PatentIn/WordPerfect

<210> 1  
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 <212> DNA  
 <213> Homo sapiens

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<221> CDS  
 <222> (3)...(1715)  
 <223> product is Poly ADP Ribose Polymerase; from brain tissue

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gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct 239  
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Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu	
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cag ttc aac aac aac aag tac tat ctg att cag cta tta gaa gat gat	383
Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp	
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gcc cag agg aac ttc agt gtt tgg atg aga tgg ggc cga gtt ggg aaa	431
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 <213> Homo sapiens

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Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu Arg		
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Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu Glu		
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 <222> (242)...(1843)  
 <223> product is Poly ADP Ribose Polymerase; from uterus tissue

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Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys	
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Gln	Gln	Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	
225						230				235						
ctg	aaa	ggc	ccc	acg	gat	ggt	ggc	caa	agc	ctg	gag	gag	ctg	tcc	tca	1006
Leu	Lys	Gly	Pro	Thr	Asp	Gly	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	
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Pro	Ile	Asn	Ser	Pro	Glu	Leu	Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	
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Cys	Pro	Thr	Leu	Gln	His	Ile	Trp	Lys	Val	Asn	Gln	Glu	Gly	Glu		
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His	Gly	Thr	Asn	Met	Ala	Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	
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Ala	Ser	Glu	Asn	Ser	Lys	Ser	Ala	Gly	Tyr	Val	Ile	Gly	Met	Lys	Cys	

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<213> Homo sapiens

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Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe Thr  
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Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His  
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Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg  
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Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala  
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Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg  
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Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln  
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<212> DNA

<213> Homo sapiens

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&lt;222&gt; (221)...(1843)

&lt;223&gt; product is Poly ADP Ribose Polymerase; from uterus tissue

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	atg tcc ctg ctt ttc	Met Ser Leu Leu Phe	
	1 5		
ttg gcc atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct			283
Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro			
10	15	20	
gag aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc			331
Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg			
25	30	35	
tcc acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc			379
Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile			
40	45	50	
cgc gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg			427
Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val			
55	60	65	
tat gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac			475
Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn			
70	75	80	85
aac aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc			523
Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe			
90	95	100	
ttc acc tgc tgg aac cgc tgg ggc cgt gtg gga gag gtc ggc cag tca			571
Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser			
105	110	115	
aag atc aac cac ttc aca agg sta gaa gat gca aag aag gac ttt gag			619
Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu			
120	125	130	
aag aaa ttt cgg gaa aag acc aag aac aac tgg gca gag cgg gac cac			667
Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His			
135	140	145	

ttt gtg tct cac ccg ggc aag tac aca ctt atc gaa gta cag gca gag	715
Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu	
150 155 160 165	
gat gag gcc cag gaa gct gtg gtg aag gtg gac aga ggc cca gtg agg	763
Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg	
170 175 180	
act gtg act aag cgg gtg cag ccc tgc tcc ctg gac cca gcc acg cag	811
Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln	
185 190 195	
aag ctc atc act aac atc ttc agc aag gag atg ttc aag aac acc atg	859
Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met	
200 205 210	
gcc ctc atg gac ctg gat gtg aag aag atg ccc ctg gga aag ctg agc	907
Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser	
215 220 225	
aag caa cag att gca cgg ggt ttc gag gcc ttg gag gcg ctg gag gag	955
Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu	
230 235 240 245	
gcc ctg aaa ggc ccc acg gat ggt ggc caa agc ctg gag gag ctg tcc	1003
Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser	
250 255 260	
tca cac ttt tac acc gtc atc ccg cac aac ttc ggc cac agc cag ccc	1051
Ser His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro	
265 270 275	
ccg ccc atc aat tcc cct gag ctt ctg cag gcc aag aag gac atg ctg	1099
Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu	
280 285 290	
ctg gtg ctg gcg gac atc gag ctg gcc cag gcc ctg cag gca gtc tct	1147
Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser	
295 300 305	
gag cag gag aag acg gtg gag gag gtg cca cac ccc ctg gac cga gac	1195
Glu Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp	
310 315 320 325	
tac cag ctt ctc aag tgc cag ctg cag cta gac tct gga gca cct	1243
Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro	
330 335 340	
gag tac aag gtg ata cag acc tac tta gaa cag act ggc agc aac cac	1291
Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His	
345 350 355	
agg tgc cct aca ctt caa cac atc tgg aaa gta aac caa gaa ggg gag	1339

Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu			
360	365	370	
gaa gac aga ttc cag gcc cac tcc aaa ctg ggt aat cgg aag ctg ctg			1387
Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu			
375	380	385	
tgg cat ggc acc aac atg gcc gtg gtg gcc gcc atc ctc act agt ggg			1435
Trp His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly			
390	395	400	405
ctc cgc atc atg cca cat tct ggt ggg cgt gtt ggc aag ggc atc tac			1483
Leu Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr			
410	415	420	
ttt gcc tca gag aac agc aag tca gct gga tat gtt att ggc atg aag			1531
Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys			
425	430	435	
tgt ggg gcc cac cat gtc ggc tac atg ttc ctg ggt gag gtg gcc ctg			1579
Cys Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu			
440	445	450	
ggc aga gag cac cat atc aac acg gac aac ccc agc ttg aag agc cca			1627
Gly Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro			
455	460	465	
cct cct ggc ttc gac agt gtc att gcc cga ggc cac acc gag cct gat			1675
Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp			
470	475	480	485
ccg acc cag gac act gag ttg gag ctg gat ggc cag caa gtg gtg gtg			1723
Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val			
490	495	500	
ccc cag ggc cag cct gtg ccc tgc cca gag ttc agc agc tcc aca ttc			1771
Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Thr Phe			
505	510	515	
tcc cag agc gag tac ctc atc tac cag gag agc cag tgt cgc ctg cgc			1819
Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg			
520	525	530	
tac ctg ctg gag gtc cac ctc tga gtgccccccc tgtccccccgg ggtcctgcaa			1873
Tyr Leu Leu Glu Val His Leu			
535	540		
ggctggactg tcatcttcaa tcatcctgcc catctctggt accccatat cactcctttt			1933
tttcaagaat acaatacggt gttgttaact atagtcacca tgctgtacaa gatccctgaa			1993
cttatgcctc ctaactgaaa tttgtattc tttgacacat ctgccccagtc cctctcctcc			2053

cagccccatgg taaccagcat ttgactctt acttgtataa gggcagctt tataggcc	2113
acatgttaagt gagatcatgc agtgtttgtc tttctgtgcc tggcttattt cactcagcat	2173
aatgtgcacc gggttcaccc atgtttcat aaatgacaag atttcctcct taaaaaaaaa	2233
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa	2265

<210> 6  
 <211> 540  
 <212> PRT  
 <213> Homo sapiens

<400> 6

Met Ser Leu Leu Phe Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val			
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Gln Thr Glu Gly Pro Glu Lys Lys Gly Arg Gln Ala Gly Arg Glu		
20	25	30

Glu Asp Pro Phe Arg Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala		
35	40	45

Glu Lys Arg Ile Ile Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn		
50	55	60

Pro Gly Thr Gln Val Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr			
65	70	75	80

Asn Ile Glu Asn Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln		
85	90	95

Asp Ser Asn Arg Phe Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly		
100	105	110

Glu Val Gly Gln Ser Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala		
115	120	125

Lys Lys Asp Phe Glu Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp		
130	135	140

Ala Glu Arg Asp His Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile			
145	150	155	160

Glu Val Gln Ala Glu Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp		
165	170	175

Arg Gly Pro Val Arg Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu		
180	185	190

Asp Pro Ala Thr Gln Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met

195	200	205
Phe Lys Asn Thr Met Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro		
210	215	220
Leu Gly Lys Leu Ser Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu		
225	230	235
Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser		
245	250	255
Leu Glu Glu Leu Ser Ser His Phe Tyr Thr Val Ile Pro His Asn Phe		
260	265	270
Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala		
275	280	285
Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala		
290	295	300
Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His		
305	310	315
Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu		
325	330	335
Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln		
340	345	350
Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val		
355	360	365
Asn Gln Glu Gly Glu Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly		
370	375	380
Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala		
385	390	395
Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val		
405	410	415
Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr		
420	425	430
Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu		
435	440	445
Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro		
450	455	460
Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly		
465	470	475

His Thr Glu Pro Asp Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly  
 485 490 495

Gln Gln Val Val Val Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe  
 500 505 510

Ser Ser Ser Thr Phe Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser  
 515 520 525

Gln Cys Arg Leu Arg Tyr Leu Leu Glu Val His Leu  
 530 535 540

<210> 7

<211> 1740

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (112)...(1710)

<400> 7

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 agggtgtggca gaactgacgg gatctaagct tctgcataatc tgaggagaac c atg gct 117  
 Met Ala  
 1

cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag cag cga 165  
 Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg  
 5 10 15

caa ggg aca gag gag gac ttc cgg tcc act gcc gag gct ctc 213  
 Gln Gly Thr Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu  
 20 25 30

aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc tca tgt 261  
 Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys  
 35 40 45 50

cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat gac tgt 309  
 Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys  
 55 60 65

acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc tat att 357  
 Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Lys Phe Tyr Ile  
 70 75 80

atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat cgc tgg 405  
 Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp  
 85 90 95

ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc acc acc tgc	453
Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys	
100 105 110	
ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag aag act	501
Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu Lys Thr	
115 120 125 130	
aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc aac aag	549
Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys	
135 140 145	
tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag gct gta	597
Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val	
150 155 160	
gtg aag gcc tta tct ccc cag gtg gac agc ggc cct gtg agg acc gtg	645
Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val	
165 170 175	
gtc aag ccc tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac	693
Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn	
180 185 190	
atc ttc agc aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg	741
Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu	
195 200 205 210	
gat gtg aag aag atg ccc ttg gga aag ctg acc aag cag cag att gcc	789
Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala	
215 220 225	
cgt ggc ttc gag gcc ttg gaa gct cta gag gag gcc atg aaa aac ccc	837
Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro	
230 235 240	
aca ggg gat ggc cag agc ctg gaa gag ctc tcc tgc ttc tac act	885
Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr	
245 250 255	
gtc atc cca cac aac ttc ggc cgc agc cga ccc ccg ccc atc aac tcc	933
Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser	
260 265 270	
cct gat gtg ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac	981
Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp	
275 280 285 290	
atc gag ttg gcg cag acc ttg cag gca gcc cct ggg gag gag gag gag	1029
Il Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu	
295 300 305	
aaa gtg gaa gag gtg cca cac cca ctg gat cga gac tac cag ctc ctc	1077

Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu			
310	315	320	
agg tgc cag ctt caa ctg ctg gac tcc ggg gag tcc gag tac aag gca			1125
Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala			
325	330	335	
ata cag acc tac ctg aaa cag act ggc aac agc tac agg tgc cca aac			1173
Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn			
340	345	350	
ctg cgg cat gtt tgg aaa gtg aac cga gaa ggg gag gga gac agg ttc			1221
Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe			
355	360	365	370
cag gcc cac tcc aaa ctg ggc aat cgg agg ctg ctg tgg cac ggc acc			1269
Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr			
375	380	385	
aat gtg gcc gtg gtg gct gcc atc ctc acc agt ggg ctc cga atc atg			1317
Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met			
390	395	400	
cca cac tcg ggt ggt cgt gtt ggc aag ggt att tat ttt gcc tct gag			1365
Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu			
405	410	415	
aac agc aag tca gct ggc tat gtt acc acc atg cac tgt ggg ggc cac			1413
Asn Ser Lys Ser Ala Gly Tyr Val Thr Met His Cys Gly Gly His			
420	425	430	
cag gtg ggc tac atg ttc ctg ggc gag gtg gcc ctc ggc aaa gag cac			1461
Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His			
435	440	445	450
cac atc acc atc gat gac ccc agc ttg aag agt cca ccc cct ggc ttt			1509
His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe			
455	460	465	
gac agc gtc atc gcc cga ggc caa acc gag ccg gat ccc gcc cag gac			1557
Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp			
470	475	480	
att gaa ctt gaa ctg gat ggg cag ccg gtg gtg ccc caa ggc ccg			1605
Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro			
485	490	495	
cct gtg cag tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa			1653
Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu			
500	505	510	
tac ctc ata tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag			1701
Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu			

515

520

525

530

att cac ctc taagctgctt gccctcccta ggtccaaagcc  
 Ile His Leu

1740

<210> 8  
 <211> 533  
 <212> PRT  
 <213> Mus musculus

&lt;400&gt; 8

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys  
 1 5 10 15

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu  
 20 25 30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro  
 35 40 45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr  
 50 55 60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Lys Phe  
 65 70 75 80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn  
 85 90 95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe  
 100 105 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu  
 115 120 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro  
 130 135 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu  
 145 150 155 160

Ala Val Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg  
 165 170 175

Thr Val Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile  
 180 185 190

Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met  
 195 200 205

Asn Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln

210

215

220

Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys  
 225 230 235 240

Asn Pro Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe  
 245 250 255

Tyr Thr Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile  
 260 265 270

Asn Ser Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu  
 275 280 285

Ala Asp Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu  
 290 295 300

Glu Glu Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln  
 305 310 315 320

Leu Leu Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr  
 325 330 335

Lys Ala Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys  
 340 345 350

Pro Asn Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp  
 355 360 365

Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His  
 370 375 380

Gly Thr Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg  
 385 390 395 400

Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala  
 405 410 415

Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly  
 420 425 430

Gly His Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys  
 435 440 445

Glu His His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro  
 450 455 460

Gly Phe Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala  
 465 470 475 480

Gln Asp Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln  
 485 490 495

Gly Pro Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln  
 500 505 510

Ser Glu Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu  
 515 520 525

Leu Glu Ile His Leu  
 530

<210> 9  
 <211> 1587  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(1584)

<400> 9

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 Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys  
 1 5 10 15

cag cga caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag 96  
 Gln Arg Gln Gly Thr Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu  
 20 25 30

gct ctc aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc 144  
 Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro  
 35 40 45

tca tgt cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat 192  
 Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr  
 50 55 60

gac tgt acc ctg aac cag acc aac atc ggc aac aac aac aag ttc 240  
 Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Lys Phe  
 65 70 75 80

tat att atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat 288  
 Tyr Ile Ile Gln Leu Leu Glu Gly Ser Arg Phe Phe Cys Trp Asn  
 85 90 95

cgc tgg ggc cgc gtc gga gag gtc ggc cag agc aag atg aac cac ttc 336  
 Arg Trp Gly Arg Val Gly Glu Val Gln Ser Lys Met Asn His Phe  
 100 105 110

acc tgc ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag 384  
 Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu  
 115 120 125

aag act aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro 130 135 140	432
aac aag tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu 145 150 155 160	480
gct gta gtg aag gtg gac agc ggc cct gtg agg acc gtc aag ccc Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro 165 170 175	528
tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac atc ttc agc Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser 180 185 190	576
aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg gat gtg aag Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys 195 200 205	624
aag atg ccc ttg gga aag ctg acc aag cag cag att gcc cgt ggc ttc Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe 210 215 220	672
gag gcc ttg gaa gct cta gag gag gcc atg aaa aac ccc aca ggg gat Glu Ala Leu Glu Ala Leu Glu Ala Met Lys Asn Pro Thr Gly Asp 225 230 235 240	720
ggc cag agc ctg gaa gag ctc tcc tcc tgc ttc tac act gtc atc cca Gly Gln Ser Leu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro 245 250 255	768
cac aac ttc ggc cgc agc cga ccc ccg ccc atc aac tcc cct gat gtg His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val 260 265 270	816
ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac atc gag ttg Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu 275 280 285	864
gcg cag acc ttg cag gca gcc cct ggg gag gag gag gag aaa gtg gaa Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Lys Val Glu 290 295 300	912
gag gtg cca cac cca ctg gat cga gac tac cag ctc ctc agg tgc cag Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln 305 310 315 320	960
ctt caa ctg ctg gac tcc ggg gag tcc gag tac aag gca ata cag acc Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr 325 330 335	1008
tac ctg aaa cag act ggc aac agc tac agg tgc cca aac ctg cgg cat	1056

Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His			
340	345	350	
gtt tgg aaa gtg aac cga gaa ggg gag gga gac agg ttc cag gcc cac			1104
Val Trp Lys Val Asn Arg Glu Gly Glu Asp Arg Phe Gln Ala His			
355	360	365	
tcc aaa ctg ggc aat cgg agg ctg ctg tgg cac ggc acc aat gtg gcc			1152
Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala			
370	375	380	
gtg gtg gct gcc atc ctc acc agt ggg ctc cga atc atg cca cac tcg			1200
Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser			
385	390	395	400
ggt ggt cgt gtt ggc aag ggt att tat ttt gcc tct gag aac agc aag			1248
Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys			
405	410	415	
tca gct ggc tat gtt acc acc atg cac tgt ggg ggc cac cag gtg ggc			1296
Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly			
420	425	430	
tac atg ttc ctg ggc gag gtg gcc ctc ggc aaa gag cac cac atc acc			1344
Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr			
435	440	445	
atc gat gac ccc agc ttg aag agt cca ccc cct ggc ttt gac agc gtc			1392
Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val			
450	455	460	
atc gcc cga ggc caa acc gag ccg gat ccc gcc cag gac att gaa ctt			1440
Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu			
465	470	475	480
gaa ctg gat ggg cag ccg gtg gtg ccc caa ggc ccg cct gtg cag			1488
Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln			
485	490	495	
tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa tac ctc ata			1536
Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile			
500	505	510	
tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag att cac ctc			1584
Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu			
515	520	525	
taa			1587

<210> 10  
<211> 528  
<212> PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 10

Met	Ala	Pro	Lys	Arg	Lys	Ala	Ser	Val	Gln	Thr	Glu	Gly	Ser	Lys	Lys
1			5			10			15						

Gln	Arg	Gln	Gly	Thr	Glu	Glu	Asp	Ser	Phe	Arg	Ser	Thr	Ala	Glu	
20				25					30						

Ala	Leu	Arg	Ala	Ala	Pro	Ala	Asp	Asn	Arg	Val	Ile	Arg	Val	Asp	Pro
35					40				45						

Ser	Cys	Pro	Phe	Ser	Arg	Asn	Pro	Gly	Ile	Gln	Val	His	Glu	Asp	Tyr
50				55				60							

Asp	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Gly	Asn	Asn	Asn	Lys	Phe	
65				70				75					80		

Tyr	Ile	Ile	Gln	Leu	Leu	Glu	Glu	Gly	Ser	Arg	Phe	Phe	Cys	Trp	Asn
85						90				95					

Arg	Trp	Gly	Arg	Val	Gly	Glu	Val	Gly	Gln	Ser	Lys	Met	Asn	His	Phe
100					105				110						

Thr	Cys	Leu	Glu	Asp	Ala	Lys	Lys	Asp	Phe	Lys	Lys	Phe	Trp	Glu	
115					120				125						

Lys	Thr	Lys	Asn	Lys	Trp	Glu	Glu	Arg	Asp	Arg	Phe	Val	Ala	Gln	Pro
130				135				140							

Asn	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Gly	Glu	Ala	Glu	Ser	Gln	Glu
145				150				155			160				

Ala	Val	Val	Lys	Val	Asp	Ser	Gly	Pro	Val	Arg	Thr	Val	Val	Lys	Pro
165					170				175						

Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	Asn	Leu	Ile	Thr	Asn	Ile	Phe	Ser
180						185				190					

Lys	Glu	Met	Phe	Lys	Asn	Ala	Met	Thr	Leu	Met	Asn	Leu	Asp	Val	Lys
195					200				205						

Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln	Ile	Ala	Arg	Gly	Phe
210					215				220						

Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys	Asn	Pro	Thr	Gly	Asp
225					230				235			240			

Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe	Tyr	Thr	Val	Ile	Pro
245					250				255						

His	Asn	Phe	Gly	Arg	Ser	Arg	Pro	Pro	Pro	Ile	Asn	Ser	Pro	Asp	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

260

265

270

Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu  
 275 280 285

Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Lys Val Glu  
 290 295 300

Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln  
 305 310 315 320

Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr  
 325 330 335

Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His  
 340 345 350

Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His  
 355 360 365

Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala  
 370 375 380

Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser  
 385 390 395 400

Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys  
 405 410 415

Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly  
 420 425 430

Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr  
 435 440 445

Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val  
 450 455 460

Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu  
 465 470 475 480

Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln  
 485 490 495

Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile  
 500 505 510

Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu  
 515 520 525

<212> PRT  
 <213> artificial sequence

<220>  
 <223> NAD+ binding domain

<220>  
 <221> VARIANT  
 <222> (2)...(6), (9)...(11)  
 <223> any amino acid; residues 3 to 6 may be present or absent

<220>  
 <221> VARIANT  
 <222> (7)  
 <223> amino acid residue 7 is either Ser or Thr

<400> 11

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Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly Ile Tyr  
 1 5 10 15

Phe Ala

<210> 12  
 <211> 25  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> NAD+ binding domain

<220>  
 <221> VARIANT  
 <222> (1), (14)  
 <223> amino acid residues 1 and 14 are either Ser or Thr

<220>  
 <221> VARIANT  
 <222> (2), (7), (9)...(13), (16)...(18)  
 <223> may be any amino acid; 10-13 may be present or absent

<220>  
 <221> VARIANT  
 <222> (6)  
 <223> amino acid residue 6 is either Ile or Val

<400> 12

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Xaa Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa  
 1 5 10 15

Xaa Xaa Gly Lys Gly Ile Tyr Phe Ala

20

25

<210> 13  
 <211> 49  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> NAD+ binding domain

<220>  
 <221> VARIANT  
 <222> (6), (16), (29)  
 <223> Ser or Thr

<220>  
 <221> VARIANT  
 <222> (7)...(13), (17), (22), (24)...(28), (31)...(33), (41)...(43), (48)  
 <223> may be any amino acid; residues 25-28 may be present or absent

<220>  
 <221> VARIANT  
 <222> 21  
 <223> Ile or Val

<400> 13

Leu Leu Trp His Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Leu Xaa  
 1 5 10 15

Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa  
 20 25 30

Xaa Gly Lys Gly Ile Tyr Phe Ala Xaa Xaa Xaa Ser Lys Ser Ala Xaa  
 35 40 45

Tyr

<210> 14  
 <211> 22  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> leucine zipper motif

<220>  
 <221> VARIANT  
 <222> (1)  
 <223> Leu or Val

<220>  
 <221> VARIANT  
 <222> (2)...(7), (9)...(14), (16)...(21)  
 <223> may be any amino acid

<400> 14

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu  
 20

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<210> 15  
 <211> 37  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> part-sequence motif 1

<220>  
 <221> VARIANT  
 <222> (21)  
 <223> Asp or Glu

<220>  
 <221> VARIANT  
 <222> (2)...(10), (12)...(13), (15)...(16), (20), (22)...(32)  
 <223> may be any amino acid; residue 32 may be present or absent

<400> 15

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Tyr Xaa Xaa  
 1 5 10 15

Gln Leu Leu Xaa  
 20 25 30

Trp Gly Arg Val Gly  
 35

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<210> 16  
 <211> 29  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> part-sequence motif 2

<220>

&lt;221&gt; VARIANT

<222> (2)...(4), (6), (8)...(11), (14), (16), (18)...(22), (24)...(26), (28)  
<223> may be any amino acid

&lt;400&gt; 16

Ala Xaa Xaa Xaa Phe Xaa Lys Xaa Xaa Xaa Xaa Lys Thr Xaa Asn Xaa  
1 5 10 15Trp Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Pro Xaa Lys  
20 25

&lt;210&gt; 17

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

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<220>

&lt;223&gt; part-sequence motif 3

&lt;220&gt;

&lt;221&gt; VARIANT

<222> (2), (5)...(6), (8)...(16), (18)...(27), (33)...(35), (38)...(43)  
<223> may be any amino acid

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (4)

&lt;223&gt; Ile or Leu

&lt;400&gt; 17

Gln Xaa Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Leu Gly Lys Leu  
20 25 30Xaa Xaa Xaa Gln Ile Xaa Xaa Xaa Xaa Xaa Xaa Leu  
35 40

&lt;210&gt; 18

&lt;211&gt; 15

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<212> PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; part-sequence motif 4

&lt;220&gt;

&lt;221&gt; VARIANT

<222> (4), (8), (11)...(13)  
<223> may be any amino acid

<400> 18

Phe Tyr Thr Xaa Ile Pro His Xaa Phe Gly Xaa Xaa Xaa Pro Pro  
1 5 10 15

<210> 19  
<211> 17  
<212> PRT  
<213> artificial sequence

<220>  
<223> part-sequence motif 5

<220>  
~~<221> VARIANT~~

<222> (2)...(4), (6)...(7), (9), (13), (15)...(16)  
<223> may be any amino acid

<400> 19

Lys Xaa Xaa Xaa Leu Xaa Xaa Leu Xaa Asp Ile Glu Xaa Ala Xaa Xaa  
1 5 10 15

Leu

<210> 20  
<211> 11  
<212> PRT  
<213> artificial sequence

<220>  
<223> part-sequence motif 6

<220>  
~~<221> VARIANT~~  
<222> (2)...(4), (6)  
<223> may be any amino acid

<400> 20

Gly Xaa Xaa Xaa Leu Xaa Glu Val Ala Leu Gly  
1 5 10

<210> 21  
<211> 28

<212> PRT  
 <213> artificial sequence

<220>  
 <223> part-sequence motif 7

<220>  
 <221> VARIANT  
 <222> (2)...(3), (5)...(8), (10)...(12), (14)...(22), (24), (26)...(27)  
 <223> may be any amino acid; residues 21 and 22 may be present or absent

<400> 21

Gly Xaa Xaa Ser Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Gly Xaa Xaa Val  
 20 25

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<210> 22  
 <211> 16  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> part-sequence motif 8

<220>  
 <221> VARIANT  
 <222> (2)  
 <223> Tyr or Phe

<220>  
 <221> VARIANT  
 <222> (3)...(4), (6)...(8), (10)...(13)  
 <223> may be any amino acid

<400> 22

Glu Xaa Xaa Xaa Tyr Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Tyr Leu Leu  
 1 5 10 15

---

<210> 23  
 <211> 20  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> synthetic sequence for antibody production

<400> 23

Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala  
1 5 10 15

Leu Asn Glu Ser  
20

<210> 24  
<211> 20  
<212> PRT  
<213> artificial sequence

<220>  
<223> synthetic sequence for antibody production

---

<400> 24

Lys Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg  
1 5 10 15

Asn Leu His Cys  
20

<210> 25  
<211> 21  
<212> PRT  
<213> artificial sequence

<220>  
<223> synthetic sequence for antibody production

<400> 25

Cys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr  
1 5 10 15

Ala Glu Ala Leu Lys  
20

<210> 26  
<211> 20  
<212> PRT  
<213> artificial sequence

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<220>  
<223> synthetic sequence for antibody production

<400> 26

Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu  
1 5 10 15

Glu Ala Leu Lys  
20

<210> 27  
<211> 19  
<212> PRT  
<213> artificial sequence

<220>  
<223> synthetic sequence for antibody production

<400> 27

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu  
1 5 10 15

Ala Leu Lys

<210> 28  
<211> 19  
<212> PRT  
<213> Mus musculus

<400> 28

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu  
1 5 10 15

Ala Met Lys

<210> 29  
<211> 7  
<212> PRT  
<213> artificial sequence

<220>  
<223> NAD+ binding domain

<220>  
<221> VARIANT  
<222> (2)...(4)  
<223> may be any amino acid residue

<400> 29

Gly Xaa Xaa Xaa Gly Lys Gly  
1 5

<210> 30

<211> 38  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PARP zinc finger sequence motif

<220>  
 <221> VARIANT  
 <222> (2)...(3), (5)...(34), (36)...(37)  
 <223> may be any amino acid; residues 33 and 34 may be present or absent

<400> 30

Cys Xaa Xaa Cys Xaa  
 1 5 10 15

Xaa  
 20 25 30

Xaa Xaa His Xaa Xaa Cys  
 35

<210> 31  
 <211> 10  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 31

Ala Ala Val Leu Asp Gln Trp Ile Pro Asp  
 1 5 10

<210> 32  
 <211> 39  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(39)

<400> 32

gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg  
 Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser  
 1 5 10

39

<210> 33  
 <211> 13

<212> PRT

<213> Homo sapiens

<400> 33

Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser  
1 5 10

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